THE OBO FOUNDRY – A FAMILY OF HIGH QUALITY INTEROPERABLE REFERENCE ONTOLOGIES

Neuhaus, Fabian[1]; Smith, Barry[1]
[1]University at Buffalo, Buffalo, NY
Keywords: Ontologies, Best Practices, Bioinformatics

The members of the National Center for Biomedical Ontology have expertise in philosophy, knowledge representation, informatics, and in the development of biomedical ontology resources as well as ontology-related software. Our center does not only use this expertise to produce resources and tools for the biomedical community, but also in disseminating its know-how by working closely with our colleagues in clinical medicine and in the life sciences. One aspect of our dissemination activities are workshops that are designed to reach out to researchers who themselves are engaged in the modeling of biomedical content and could benefit from ontology related technologies, but are not familiar with them. In addition we are propagating best practices and quality control methods that will improve the utility, increase the lasting value of biomedical ontologies that are developed, and allow for greater interoperability between them.

The creation of the OBO Foundry in the spring of 2006 was an important step in this direction. The goal of this effort is to establish a family of interoperable, high quality reference ontologies to be used in the annotation of biomedical data. The Foundry is a collaborative experiment, involving a group of ontology developers who have agreed in advance to the adoption of a growing set of principles specifying best practices in ontology development. The Foundry is a standards-based initiative that is prospective in the sense that it is designed both to ensure the gradual improvement of existing ontologies and to provide guidance for ontology creation. The existing ontologies will be iteratively refined until they are able to serve the function of a reference ontology for their allocated domain while at the same time maintaining backwards compatibility with the annotation resources already in common use. Three new ontologies – the Protein and RNA Ontologies, and the Functional Genomics Investigation Ontology – are already being created in the terms of the Foundry. The following are candidate members of the Foundry or are under review:

Candidates	Under review
GO Gene Ontology	Disease Ontology
CL Cell Ontology	SO Sequence Ontology
ChEBI Chemical Ontology	Mammalian Phenotype Ontology
PATO Phenotype Ontology	Plant Trait Ontology
FMA Foundational Model of Anatomy	Protein Ontology
RO Relation Ontology	RnaO RNA Ontology
FuGO Functional Genomics Investigation Ontology	

E-mail: fneuhaus@buffalo.edu